5' GGT GGC GAC GAC TCC TGG AGC CCG 3'	SEQ ID NO:6
5' TTG ACA CCA GAC CAA CTG GTA ATG 3'	SEQ ID NO:7
5' GAC CGC GAT GAT GTG GCT TTG AAG AAC 3'	SEQ ID NO:8
5' GAT AGG ATC TTT AGC GAC AGC CGA 3'	SEQ ID NO:9
5' ATG GCG GCC TCT GAG TCC TGG TGG 3'	SEQ ID NO:10
5' CGG GCT GAA TGC AAT GGA GTG TGC 3'	SEQ ID NO:11
5' GAC CCC CAT TTG TGT GAC 3'	SEQ ID NO:12
5' CGA CGA CTC CTG GAG CCC G 3'	SEQ ID NO:13
5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3'	SEQ ID NO:14
5' AGC CGA CAG CGA TTT CTA GGA TAG 3'	SEQ ID NO:15
5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3'	SEQ ID NO:16
5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3'	SEQ ID NO:17
5' CAG ACG TTC TTC GCC GAG AGT CGT 3'	SEQ ID NO:18
5' CAG ACG TTC TTC GCC GAG AGT CGT CGG 3'	SEQ ID NO:19
5' CAT TTC GGG GAT TCG GGG GA 3'	SEQ ID NO:20
5' GGG GGA CGG AAC CCG GCG CT 3'	SEQ ID NO:21
5' CCC TCT ACA CTT ATC ATC TTC 3'	SEQ ID NO:22
5' CTA TCC TAG AAA TCG CTG TCG GCT 3'	SEQ ID NO:23
5' GTC ACT GGA ATT CCC TTC TCC 3'	SEQ ID NO:24
5' GGA GAA GGG AAT TCC AGT AGT GAC 3'	SEQ ID NO:25
5' GGA AAT CGC TGT CGC CTA ACC 3'	SEQ ID NO:26
5' GGT TAG GCG ACA GCG ATT TCC 3'	SEQ ID NO:27
5' GGC CAC GCG TCG ACT AGT AC 3'	SEQ ID NO:28
5' GTA ATG CAC ACTCCA TTG GC 3'	SEQ ID NO:29
5' GTA ATG CAC ACT CCA TTG 3'	SEQ ID NO:30
5' GCG CTC AGC TGG AAT TCC 3'	SEQ ID NO:31
5' GGA ATT CCA GCT GAG CGC 3'	SEQ ID NO:32
5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3'	SEQ ID NO:33
5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3'	SEQ ID NO:34
5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3'	SEQ ID NO:35
5' CCC GCT CGA GTC AGG GTG ACC GAA AAA TCA G 3'	SEQ ID NO:36

Please replace the two paragraphs beginning at line 6 on page 16 and ending at line 13 of page 16 with the following rewritten paragraphs:

- --Fig. 1 shows the nucleic acid sequence (SEQ ID NO:1) of clone T16 isolated from T47D breast cancer cDNA library.

 Initiation and termination codons of the open reading frame are indicated by dark bars;
- Fig. 2A shows a comparison of the nucleic acid sequences (upper sequence) (SEQ ID NO:2) of clone 4.7 isolated from a placenta cDNA library exhibiting normal human FTH, and the sequences (lower sequence) of clone T16 (SEQ ID NO:1) isolated from human breast cancer T47D cDNA library. Initiation and termination codons of the open reading frame are marked by dark boxes;--

Please replace the three paragraphs beginning at line 17 of page 16 and ending at line 25 of page 16 with the following rewritten paragraphs:

- --Fig. 3 shows a comparison of sequence homology between cDNA clone T16 (residues 463-671 of SEQ ID NO:1) and human mitochondrial cytochrone oxidase I DNA (SEQ ID NO:3);
- Fig. 4 shows a comparison of nucleic acid sequences between placental cDNA obtained by PCR amplification using T16 specific primers (upper sequence) (residues 24-822 of SEQ ID NO:1) and T16 cDNA sequence obtained from the T16 cDNA clone (lower sequence) (SEQ ID NO:4). Identical nucleic acid sequences are indicated by a dotted line. Initiation and termination codons are indicated by a dark bar;
- Fig. 5 shows the nucleic acid sequence and deduced amino acid sequence (SEQ ID NO:5) of the cDNA of OFF1;--

Please replace the two paragraphs beginning at line 4 of page 17 and ending at line 6 of page 17 with the following rewritten paragraphs:

--Fig. 7 shows the sequence of clone T16 (SEQ ID NO:1). Primers used for PCR are indicated in the above sequence;

Fig. 8 shows the restriction enzyme map sequence of clone T16 (SEQ ID NO:1);--

Please replace Table 1 on page 19 with the following rewritten Table 1:

Table 1
List of Primers

Name	#MR	Sequence	SEQ ID		
			NO:		
1060 F	24	5' GGT GGC GAC GAC TCC TGG AGC CCG 3'	6	75%	
1061R	24	5' TTG ACA CCA GAC CAA CTG GTA ATG 3'	7	45.80%	
17F	27	5' GAC CGC GAT GAT GTG GCT TTG AAG AAC 3'	8	52%	27618
X1.1F	24	5' GAT AGG ATC TTT AGC GAC AGC CGA 3'	9	50%	24880
X.1.1R	24	5' ATG GCG GCC TCT GAG TCC TGG TGG 3'	10	67%	
2.1F	24	5' CGG GCT GAA TGC AAT GGA GTG TGC 3'	11	58%	
3.4F	18	5' GAC CCC CAT TTG TGT GAC 3'	12	55.50%	
1060F/S	19	5' CGA CGA CTC CTG GAG CCC G 3'	13	73.70%	
1061r/Bio	. 24	5' Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3'	14	45.80%	
16X.1R	24	5' AGC CGA CAG CGA TTT CTA GGA TAG 3'	15	50%	24879
17R	27	5' GTT CTT CAA AGC CAC ATC ATC GCG GTC 3'	16	52%	27385
3'COD R	28	5' GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3'	17	50%	28313
5' NCF	24	5' CAG ACG TTC TTC GCC GAG AGT CGT 3'	18	58%	24870
4869	27	5' CAG ACG TTC TTC GCC GAG AGT CGT CGG 3'	19	63%	
NFG	20	5' CAT TTC GGG GAT TCG GGG GA 3'	20	60%	
NFGP-2	20	5' GGG GGA CGG AAC CCG GCG CT 3'	21	80%	201880
767-F	21	5' CCC TCT ACA CTT ATC ATC TTC 3'	22	43%	211616
16 - F	24	5' CTA TCC TAG AAA TCG CTG TCG GCT 3'	23	50%	241173
ECO-F	24	5' GTC ACT ACT GGA ATT CCC TTC TCC 3'	24	50%	24960
ECO-R	24	5' GGA GAA GGG AAT TCC AGT AGT GAC 3'	25	50%	24961
SPF	21	5' GGA AAT CGC TGT CGC CTA ACC 3'	26	57%	211667
SPR	21	5' GGT TAG GCG ACA GCG ATT TCC 3'	27	57%	211668
AUAP	20	5' GGC CAC GCG TCG ACT AGT AC 3'	28	65%	202738
NC-F	20	5' GTA ATG CAC ACTCCA TTG GC 3'	29	50%	203814
SNC-F	18	5' GTA ATG CAC ACT CCA TTG 3'	30	44%	181897
BNC-F	18	5' GCG CTC AGC TGG AAT TCC 3'	31	55.50%	181898
BNC-R	18	5' GGA ATT CCA GCT GAG CGC 3'	32	61.10%	181905
pGEX-F	29	5' GTG GGA TCC CCA TGA CGA CCG CGT CCA CC3'	33	67%	29391
pGEX-R1	27	5' GAC TCG AGT TAA GCC GAC AGC GAT TTC 3'	34	51.85%	27578
pGEX-R2	29	5' GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3'	35	51.70%	29396
pGEX-R3	31	5' CCCGCTCGAGTCAGGGTGACCGAAAAATCAG 3'	36	58%	31277

Please replace the paragraph beginning at line 6 on page 27 with the following rewritten paragraph:

--The expression vector (pGEX-5X-1) used for gene fusion construction was the GST Gene Fusion System (Pharmacia). The OFF1 coding region (designated as "FL", fulllength) of about 0.5 kb was prepared by PCR with the following 5' end primer:

5' $GT_{\underline{GGGATCC}}$ CCATGACGACCGCGTCCA (1-27 of SEQ ID NO:33), in order BamHI

to add a BamHI site 1 base upstream from the start codon ATG and with the 3^\prime end primer

5' CCCG CTCGAG TCA GGG TGA CCG AAA AAT CAG 3' (SEQ ID NO:36) in Xho1

order to add an Xhol site after the stop codon TAA using the PCR kit (Perkin-Elmer/Centus).--

IN THE DRAWINGS

Attached hereto are copies of Figures 1, 2A, 5,, 7 and 8 with proposed revisions marked in red. Approval of these revisions is respectfully requested.

IN THE SEQUENCE LISTING

Please substitute the attached Sequence Listing, numbered as pages 1-8 for the Sequence Listing previously submitted.